# TAXONOMY VERSUS CLADONOMY IN THE DICOT FAMILIES[1]

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## Abstract

The theoretical basis for cladistic classification into monophyletic (holophyletic) ranked taxa is fatally flawed and is promoting bad taxonomy. Biological classification that takes account of evolutionary history may be based on two main factors—lines of descent and extent of divergence represented by morphological and other characters. In taxonomy a balance must be found between lines of descent and characters, and insistence on one at the expense of the other will give unacceptable results. Much confusion has arisen in systematics from the failure to appreciate that taxonomy, which groups organisms into ranked taxa (families, genera, etc.), is essentially different from grouping them into clades. These two processes are based on conflicting hierarchies and have different methodologies and functions. For several decades, however, the cladistics movement has adopted lines of descent rather than characters as the sole basis of taxonomy, insisting that only complete clades should be recognized as taxa. But as soon as one imposes ranks on a phylogeny, one must create paraphyletic taxa. These are natural products of evolution, which should be recognized in taxonomy. When ranks are adopted without acceptance of paraphyletic taxa, taxonomic free fall sets in, and every clade sinks into those taxa to which its original ancestor is referable. The clash of hierarchies results in absurdity, extending to sinking the entire plant kingdom into one family and one genus, but this has been strangely overlooked by the cladistic side. Adoption of ranked taxa is incompatible with recognition of only complete clades. Merely because one taxon falls phylogenetically within the clade of another taxon at the same rank does not necessarily mean that it must be included in it taxonomically. New characters will have arisen during evolution, which should be taken into account. A monophyletic (= holophyletic) system recognizing only complete clades is logically possible only if ranks are abandoned, as in the PhyloCode. It may be referred to as a "cladification" and the process producing it as "cladonomy," which are quite different concepts from a "classification" and "taxonomy." In a classification we have a hierarchical series of taxa at different ranks, while in a cladification we merely have a hierarchy of clades nesting within successively bigger clades. Cladistic taxonomy is particularly nonsensical in paleobotany, where our Linnaean taxonomic system and our code of nomenclature apply just as they do for extant plants. Cladograms are not classifications, and they need critical taxonomic assessment. The great majority of users of taxonomy are interested in characters and not cladistic theory. A general purpose classification is needed, requiring acceptance of paraphyletic taxa that are defined by characters as well as lines of descent. Examples in the dicot flowering plant families are given in which cladistic principles have imposed excessive insistence on lines of descent at the expense of evolution of characters, producing what many regard as bad taxonomy.

*Key words:* Cladification, cladistics, cladograms, cladonomy, classification, evolution, flowering plant families, hierarchies, paraphyly, taxonomy.

It has been over 150 years since Darwin published *On the Origin of Species*, and it will be surprising to some observers that in the 21st century there is still heated disagreement on how the theory of evolution affects the classification of plants and animals. I entered the fray of this argument the best part of 20 years ago and have somehow survived all the slings and arrows that have been sent my way since. I said some years ago that this is the most important issue under debate in biological systematics today, and I feel that nobody has ever seriously challenged the critical views on cladistics that I and many other taxonomists have put forward. Open discussion is needed to resolve this persistent aggravating problem.

## Two Different Processes

There is a major schism between two schools of thought on how we should derive a classification from the evolutionary history of a group. Those persuaded by the cladistics movement emphasize past lines of descent as the only basis for classification. They insist that all taxa must be monophyletic, that is, they should be complete clades, so one family cannot have evolved from within another family because that would be an incomplete clade and so paraphyletic. Their units are then defined by lines of descent (ancestry) rather than by characters. The result is a "cladification," and in my title I have called the process "cladonomy," having adopted these terms 15 years ago (Brummitt, 1997) from the late and great

[1] Based on the text (with some additions) of a video presentation given to the XVIII International Botanical Congress in Melbourne in July 2011.

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doi: 10.3417/2012089

zoologist Ernst Mayr. The other school allows that *characters* are important and have changed through evolution, so that one taxon may have *evolved* from within others at the same and presumably lower ranks. This enables us to produce a "classification," taking into account evolution of characters, as distinct from a "cladification" based only on lines of descent.

"Taxonomy" is the naming of taxa while "cladonomy" is the naming of clades, and "cladistic taxonomy" is an oxymoron (Knox, 1998: 5). In recent decades the process of recognizing groups according to their descent *and* their characters has become known as "evolutionary taxonomy," a very appropriate term also popularized by Ernst Mayr (see Mayr & Ashlock, 1991, and references therein, and a historical review by Ashlock, 1974). Stuessy (2006) has noted that the term "phyletics" also takes into account the degree of divergence, whereas "cladistics" uses only the branching pattern. Hörandl (2006) has emphasized the difference between a classification based on evolution of characters and one based on cladistic theory, and she titled her article, "Neglecting Evolution Is Bad Taxonomy" (Hörandl, 2007). Cladistics indeed defines taxa solely by their ancestry and ignores the evolution of characters (Stuessy & König, 2009). In broad reviews of the subject, Stuessy (2009) and Hörandl and Stuessy (2010) have, like other authors, stressed that paraphyletic taxa defined by descent *and* characters are natural units in evolution and are not only desirable but indeed inevitable in taxonomy.

## Basic Concepts Confused

So how is it that these two schools of thought have developed alongside each other? Following the publication of Hennig's influential ideas on cladistic analysis (1966), the view was widely propagated that this must be the basis of modern taxonomy. Many philosophical papers of the 1960s to 1990s were concerned with definitions and how Hennig's methods could recreate actual phylogenetic history in terms of clades—see, for example, Nelson (1971), Farris (1974), Platnick (1979), or Patterson (1982). All commentators on the cladistic side apparently made a fatal assumption that there is only one way to chop up a phylogenetic tree, and they concluded that all taxa must be monophyletic—that is, complete clades. But they did not address the question of how to produce a classification of clades into ranked taxa without any being paraphyletic. In fact, ranks were never even mentioned. So application of the formal taxonomic hierarchy to a phylogeny was not considered at all. Although this is fundamental to taxonomy, it has been completely ignored in a large body of theoretical literature on cladistics up to the present day. But as soon as one applies ranks to a phylogenetic tree in order to produce a classification, one must create paraphyletic taxa. Every suprageneric taxon accepted has apparently descended from something recognizable at around species level and must make another taxon paraphyletic. If paraphyletic taxa are not accepted, every clade (including the entire plant kingdom) will sink into those taxa (family, genus, perhaps species) to which their ancestor is referred. The phylogenetic tree can thus be chopped up according to evolution of characters, creating a taxonomy, in a quite different way from recognizing only complete clades. Evolution of ranked taxa is paraphyly all the way. The hierarchy of descent is not the same as the taxonomic hierarchy. It was left to De Queiroz and Gauthier (1992) to state the obvious conclusion that cladistic classification is incompatible with ranked taxa. It is a simple point, but failure to recognize the difference between taxonomy and cladonomy is the cause of many of our current problems in systematics.

But as new methods of data analysis developed driven by computer programs, the new thinking of cladistics became fashionable and was widely but uncritically accepted by many as the correct and only way forward for taxonomy. It was argued that lines of descent are objective matters of historical fact, and, even though they are impossible to observe directly, this must take precedence over use of *characters* as formerly adopted as the basis of taxonomy. It is true that traditional classification has an element of subjectivity in defining taxa according to characters, but at least it can be based on direct observation. But all classification is subjective in assignation of ranks to taxa, and evolutionary taxonomy is no more subjective than is "cladistic taxonomy." In cladistic thinking, all taxa must be monophyletic (= holophyletic, i.e., complete clades), and the view that paraphyletic taxa (incomplete clades reflecting evolution of characters) are anathema was widely—but not universally—accepted.

It is fundamental to the present discussion that taxonomy and cladonomy are quite different processes with different functions. Taxa are grades showing maximum correlation of characters and are essentially different from clades, and the two concepts cannot be combined in one system. They are logically incompatible with each other, though they may often coincide since many recently evolved taxa are also clades. The differences between grades and clades have long been apparent in discussions of taxonomic theory where these contrasting concepts have been recognized

(Davis & Heywood, 1963; Cronquist, 1987: 2, 8–9). The Venn diagram of Brummitt (1996: fig. 1, and 2002: fig. 2) illustrates how the hierarchies of phylogeny and of classification conflict with each other and cannot be equated. In practice, we need to choose which we want according to the use to which it will be put. Ashlock (1974) has demonstrated that in phytogeographical analysis we need to adopt monophyletic groups (clades), but in creating a taxonomy this is inappropriate, and we need taxa, which inevitably create paraphyly. However, this fundamental difference was overlooked by many commentators in the cladistic scene. A quite different criterion for classification was thus introduced with very little consideration of its logical basis or the practical effects it would have. The mood of many was for a new thinking stressing ancestry at the expense of evolution of characters, but this is now seriously challenged.

## The Present Argument

We now have evolutionary taxonomy competing with "cladistic taxonomy," each with deeply entrenched lines of supporters. It is not just a matter of one way of operating being rather better than the other. It is, in my opinion, a case of one theory or principle being clearly logically **wrong** and the other logically **correct.** Evolution is an ongoing process of change through time. To divide a phylogenetic tree representing development of taxa over a period of time into families, genera, and species without any of them being descended from within another taxon at the same or lower rank is a logical absurdity. It should be obvious that, if this were accepted, no new taxa could ever have evolved. Every taxon would sink into another. No genera or families or higher taxa could be recognized, and the entire plant kingdom would sink into one family and genus. I have here referred to this phenomenon as "taxonomic free fall," having previously referred to it as "infinite regression" (Brummitt, 1996: 376). Our theory of classification will be incompatible with evolution if it cannot accommodate all the products of the evolutionary process, including fossils and other extinct plants. And if it ignores characters, it will be nonsensical to users. If it does not accept paraphyletic taxa, which are natural products of evolution defined by characters, it is surely not acceptable. **The theoretical basis for cladistic classification into monophyletic ranked taxa is fatally flawed and is promoting bad taxonomy.**

The cladistic view would require that as evolution produces wider and wider variation, the rank of the taxa that result has to be progressively lower and lower (see examples quoted below, particularly Cactaceae). How can anyone believe this? To me, it is **nonsensical**. Common sense would lead us to expect the opposite. The taxonomic hierarchy and the hierarchy of descent, which work in opposite directions, have been confused. It has been said with disarming honesty on the cladistic side (Albach et al., 2004: 429) that, if you want ranks *and* only monophyletic taxa, you must either sink taxa that are quite distinct (see many examples below, particularly Scyphostegiaceae and Lennoaceae) or split taxa where there are no appropriate characters to do so (see Portulacaceae and Scrophulariaceae below). This means that characters are ignored and taxonomy becomes nonsensical to users. There *must* be something fundamentally wrong with this. Characters are essential to taxonomy, but they are neglected in cladistic classification.

Cronquist (1987: 2) was among the first to appreciate the problems of cladistic taxonomy, pointing out that the refusal to accept paraphyletic taxa is a fatal flaw in the theory behind it. He noted that such taxonomy assigns ranks to organisms "entirely on the basis of recency of common descent" while "the *amount* of divergence scarcely enters the picture." At an Association for the Taxonomic Study of the Flora of Tropical Africa (AETFAT) Congress in 1994, the logical impossibility of combining monophyly with ranked taxa was emphasized again (Brummitt, 1996; but see also Schrire & Lewis, 1996). Some 15 years ago, Sosef (1997) referred to the inevitability of supraspecific paraphyletic taxa. In the same year Stuessy (1997) pointed out that classification should be based on more than just branching patterns. Over the last quarter of a century it has been increasingly argued—often from different perspectives—that recognition of taxa based on characters is a quite different process from recognition of clades, and they should not be confused (Buck, 1986; Cronquist, 1987; Hedberg, 1995; Brummitt, 1996, 1997, 2002, 2008; Sosef, 1997; Stuessy, 1997, 2006, 2009; van Welzen, 1997; Brummitt & Sosef, 1998; Knox, 1998; Diggs & Lipscomb, 2002; Grant, 2003; Nordal & Stedje, 2005; Stace, 2005; Cullen & Walters, 2006; Hörandl, 2006, 2007, 2010; Farjon, 2007, 2009; van Wyk, 2007; Zander, 2007; Cullen in Brickell et al., 2008; Stuessy & König, 2009; Hörandl & Stuessy, 2010; Podani, 2010).

But those who are seduced by the superficial attractiveness of a system of ranked taxa that are all complete clades (i.e., containing only holophyletic groups) have been unwilling to accept that this is a logical impossibility, or they have chosen to ignore it. So the taxonomic community is now divided on a major principle. It has been said that paraphyletic

groups cannot be recognized as taxa because they have no real biological existence, but what is meant is merely that they are not complete clades, which is self-evident from their definition. Such groups are the unavoidable consequence of anagenesis in evolution, and they exist as real biological entities through their definition by characters (Hörandl & Stuessy, 2010). Claims from the cladistic side that paraphyletic groups have no defining characters (Patterson, 1982) seem strange. Such groups are just as much a reflection of how evolution has progressed as is the concept of monophyly and should be accepted in our taxonomy. Ignoring evolution of new characters is bad taxonomy (again, Hörandl, 2007).

## So What *Should* We Do?

If you insist on only monophyletic (= holophyletic) units (clades), you have to abandon ranks, and then the concept of paraphyletic taxa cannot apply. You then just have clades nesting within bigger and bigger clades. This was realized by proponents of the PhyloCode two decades ago, and De Queiroz and Gauthier (1994), in their second paper, proposed a new taxonomy with new nomenclature that abandoned ranks (see also Moore, 1998; De Queiroz & Cantino, 2001; Cantino et al., 2007). There would be no families, no genera, no binomials for species—only clades. But that is not practical taxonomy, and it has not gained general acceptance in the botanical world. The PhyloCode was logical (a good example of cladonomy), even if not practical, but cladistic taxonomy is neither logical nor practical. Those who want their classification to recognize only clades irrespective of characters are asking for something very narrowly specialized (Cronquist, 1987: 2; Stace, 2005). They should adopt the appropriate approach and abandon ranks instead of trying to replace the taxon-based classification that most users need.

In recent decades those wanting only monophyletic taxa have been boosted by the revolution in molecular systematics, and those like me on the other side of the cladistic argument have been castigated as being out of touch with modern developments. But it is not the evolutionary taxonomists who are behind in their ideas; it is the cladistic side, who have failed to respond to the logical arguments that have been advanced by their opponents. Now the tide has turned, and the thinking has moved on since the late 20th century. I am a great supporter of molecular data—so long as they are used properly. But the cladistic arguments that usually accompany molecular analyses are not driving taxonomy forward; they are putting it into reverse. As van Wyk (2007: 647) has said, "It is ironic that at a time when phylogenetic understanding is at an all time best, the usefulness of classifications has deteriorated to the point of becoming absurd." Indeed, the nearer that modern technologies bring us to reconstructing past evolution, the greater is the absurdity of cladistic classification. If we knew everything, we would have only one family and one genus.

For those who think that traditional taxonomy is just too old-fashioned to be recognized as serious science, I would note that in 1997 a formal debate at the Linnean Society of London voted heavily against cladistic theory and in favor of evolutionary taxonomy (see Brummitt, 2002: 40). In the last decade, some 170 practicing taxonomists, including many senior figures, have put their names to statements in *Taxon* opposing the cladistic line (see especially Nordal & Stedje, 2005). Most users of our taxonomy are not interested in cladistic theory; they are interested in the characters of the taxa we recognize (Cullen in Brickell et al., 2008). The practical importance of taxonomy has similarly been stressed by Diggs and Lipscomb (2002), Stace (2005), van Wyk (2007), and others. Grant (2003) has emphasized the incongruence of cladistic and taxonomic systems. Cladistic treatments of well-known groups have been considered unacceptable (Farjon, 2009). Recent arguments that have been advanced favoring the cladistic view (Nelson et al., 2003; Wiley, 2009) have been refuted (Brummitt, 2003; Stuessy & König, 2009). In a perceptive historical overview of family classification, Cullen and Walters (2006) have said that the principle of monophyly (holophyly) is now discredited and of zero value.

Similar problems are under debate in zoology, as seen in the difference of opinion over the sinking of the leeches into the earthworms (Schmelz & Timm, 2008). And even a botanist can reflect that mammals nest phylogenetically within bony fishes and so should be sunk according to cladistic theory (Brummitt, 2006). The logical and practical arguments against cladistic taxonomy at the very least demand serious consideration, but they are ignored by many, and bad taxonomy continues to pour forth.

## Phylogenies versus Cladograms

One point of view that is probably widely held on the cladistic side has been well expressed by Potter and Freudenstein (2005) and requires comment (see also Freudenstein, 1998; and response by Brummitt & Sosef, 1998). They have argued for both monophyly and ranked taxa in the same system and have rightly drawn attention to essential differences between phylogenetic trees and cladograms. Because we do not have the extinct ancestors and so cannot know the

"true underlying phylogeny" (Potter & Freudenstein, 2005: 1034), they prefer to base their classification on cladograms rather than phylogenetic trees. But cladograms do not include ancestors or a timescale, which are essential to the concepts of holophyly and paraphyly, and they do not determine the ranks of their various branches. They commonly represent taxa only at a single point in time—a synchronous classification in the terminology of Podani (2009, 2010)—since, with rare exceptions, only present-day taxa are included. A diachronous classification, by contrast, includes all extinct and living organisms, and a phylogenetic tree remains the only meaningful representation of ancestor/descendant relationships (Podani, 2010). Dealing only with cladograms means that change of characters over time, and consequently evolution of new taxa, are not revealed.

The view is sometimes put forward that, if we are dealing only with extant plants and will accept a synchronous classification, it is possible to recognize only holophyletic taxa. But this only emphasizes that cladistic theory is incompatible with the ongoing process of evolution through time. If we were concerned only with extant plants and discounting their ancestors, nothing would be paraphyletic since present-day plants have not evolved from other present-day plants. On the other hand, if cladistics postulates extinct ancestors in order to demonstrate paraphyly, then it must also postulate extinct ancestors that produce taxonomic free fall, causing all classifications to collapse into one taxon. Just because we cannot name an ancestor does not mean that ancestors did not exist or that they do not need to be considered. We should not confuse taxonomy with nomenclature. Cladograms cannot assess taxonomic significance of the development of new characters (see discussion of Scyphostegiaceae below). Podani (2010) has considered that paraphyly is a mathematical necessity in diachronous phylogenetic classification. When we consider that our principles of Linnaean classification and our code of nomenclature apply to paleobotany as well as to extant taxa, the cladistic argument is manifestly untenable.

Cladograms are not immutable since their topology may change with the inclusion of more or fewer taxa or different characters in the analysis, and indeed the same data set may give multiple cladograms. Furthermore, it is doubtful whether cladistic analysis of only extant taxa ever gives an accurate picture of past evolution as directly evidenced by fossils (Axsmith et al., 1998; Farjon, 2007; see also Hedberg, 1996). If we could build extinct plants into our cladograms that are based on extant plants, the topology would very probably change considerably. Consider, for example, what we know (or, more important, what we don't know) about the evolution of Hydrostachyaceae—see below. Should we really ignore the taxonomic importance of *characters* and derive our classification entirely from topology of diagrams that are based only on present-day taxa and probably do not accurately reflect the true underlying phylogeny (Grant, 2001; see also splitting of Flacourtiaceae, below)? Characters may, of course, be used in the production of a cladogram and may be highlighted within it, but according to cladistic theory they do not play any part in taxonomic assessment. Cladograms give useful visual impressions of phylogenetic relationships, but they do not determine ranks and are not classifications (Brummitt, 1996). They need critical taxonomic interpretation. As Stuessy (1997) and Stuessy and König (2009) have argued convincingly, we need to look beyond the topology of cladograms in producing a classification. See also Ashlock (1974: 94–97).

Phylogenetic trees, on the other hand, include a timescale and ancestors and are a better representation of actual phylogeny. But the fundamental question is not whether we should base our classification on phylogenetic trees or on cladograms. The arguments are just the same either way. The basic question is whether we can accept that one family can have evolved from within another family, one genus from within another genus, and so on. Why should that not be so? To those who believe in evolution, it would seem to be the inevitable assumption. Where else did they come from? As soon as you apply ranks to a phylogenetic tree, you must create paraphyletic taxa. **So why should we try to make all taxa holophyletic in our taxonomy?** It makes no sense. Have we had development from unicellular algae to advanced angiosperms without anything ever giving rise to a new group recognizable at the same or higher rank? The whole theory of cladistic taxonomy is in conflict with the evolution of characters and new taxa and defies natural intuition. Whether we work with phylogenies or cladograms, so-called cladistic taxonomy is unacceptable because it is incompatible with development of new taxa and with Linnaean nomenclature.

## Examples in Dicot Families[1]

All these considerations affect family concepts in the dicots. Please note that I am not talking about a

[1] Names of families and other taxa affected by the preceding discussion are here printed in boldface for ease of reference. This does not reflect any particular taxonomic conclusion.

linear sequence of families (where I am largely supportive of the latest conclusions based on molecular data); I am talking only about how the families are defined. I know nothing worth knowing about the monocots but have worked my way through the dicot families over the last 15 years. When I compared my list of dicot families with those recognized by authors accepting cladistic principles,[2] I found that there were 112 differences out of a total of about 400 families—about 25% to 30% disagreement. Not all of these were the direct result of paraphyly, since some were due merely to the associated problem of failure to take characters into account. Most are cases where cladists sink families where I would split, but in a few instances it is the other way round. I have selected a few cases to show how paraphyly or failure to recognize characters can be the major factor.

I am starting with the pantropical and Southern Hemisphere traditional family **Flacourtiaceae**. First, let me say that I have agreed that *Aphloia* (DC.) Benn. and *Berberidopsis* Hook. f. have to be taken out of Flacourtiaceae because both the molecular data and the morphological evidence support it. But then we come to *Scyphostegia* Stapf, which has long been treated as a monotypic family **Scyphostegiaceae** endemic to Borneo. It is indeed a very strange plant in its reproductive structures. The male inflorescence is compact, oblong to linear, up to 5 × 2 cm, consisting of 20 to 25 very short concentric tubular bracts, like a mini Leaning Tower of Pisa. Nestling within these short tubes are the inconspicuous male flowers, one per bract, with a green tubular perianth with three long and three short lobes, and three stamens united into a column. The female inflorescence has usually only two short concentric bracts and again a shortly tubular perianth, and the ovary has many erect elongate ovules crowded together on its floor. I wonder if you have been counting the number of important features that do not characterize traditional Flacourtiaceae—unique extraordinary inflorescences, fused perianth (as distinct from free sepals and petals), six unequal perianth lobes, only three stamens (as distinct from usually very many), a staminal column, many basal (not parietal) ovules, and so on. In discussing various suggested possible affinities of *Scyphostegia*, van Steenis (1972) commented that all recent authors agreed that it is a distinct family on its own. But cladonomy ignores characters and is based on quite different criteria from taxonomy, and cladists sink Scyphostegiaceae into the traditional concept of Flacourtiaceae. It does not matter to them how many differences there are or how conspicuous these are. If it falls within another family in their cladogram, they are very sorry—they will say—but they have to sink it. To them, characters are irrelevant. Everything depends on presumed lines of descent. You must ignore the evolution of new characters. But, again as Hörandl (2007) has said, neglecting evolution is bad taxonomy.

But there is more. The cladogram based on *rbcL* sequences presented in Chase et al. (2002) divides the 80 or so genera of traditional Flacourtiaceae into two major groups that are now treated in the cladistic literature as separate families. But only 30 out of the 80 genera were sampled, including only one species of the basal tribe Casearieae, which has 13 genera (including *Casearia* Jacq. with some 180 species). The characters quoted in the paper show no morphological support for recognizing two families, and experienced taxonomists who have worked extensively in this group tell me they see no good case for splitting the traditional family in this way. Relying solely on the topology of this cladogram does not seem to me to be necessarily good taxonomy. One wonders whether more complete sampling at the base of the tree might not hold the traditional family together.

Furthermore, in one part of the cladogram is a South African group of three monotypic genera long known as the family **Achariaceae** (see van Wyk, 1988), nesting within one half of the whole group and so sunk to tribal level. They differ markedly from traditional Flacourtiaceae in their habit (herbaceous rosettes or climbers with palmate leaves, rather than trees and shrubs), their exstipulate leaves, a strongly *gamopetalous* corolla rather than free petals, and only three to five stamens rather than usually very many. But again, despite the presence of these striking characters, cladistic theory has sunk this family, and many will consider that to be a retrograde step. Evolutionary taxonomy would allow us to assess *characters* and take our own decisions, but cladistics ignores characters and always rigidly forces us into one position, which many taxonomists would reject as being simply bad taxonomy.

But worse is to come. It turns out that the name "Achariaceae" is the earliest family name in the group, so the cladistically motivated are now obliged

[2] Cladistic views referred to here are those employed in the third system published by the Angiosperm Phylogeny Group (2009), popularly known as APG III, and Mabberley (2008), unless a different reference is given. In some cases alternative conclusions are reached by other authors. Other references to taxonomic papers are cited in the text. Where no citation is given, a useful source for many further references to the taxonomy of families mentioned, plus many illustrations, with examples and discussions of the classifications preferred here, can be found in Heywood et al. (2007).

to use that name for half the traditional Flacourts while those not so constrained keep it for the three South African genera. But when Achariaceae are demoted to become the tribe **Acharieae**, they nest within the tribe Pangieae, so that is just as paraphyletic as the broad family was. Sinking the family just transfers paraphyly to a different rank. The distinctive group long recognized as a family by evolutionary taxonomists must have a rank *lower than tribe* in cladistic classification. In the absence of the restraining effect that consideration of characters would afford, taxonomic free fall is setting in. This sort of thing is always liable to happen when we start sinking on cladistic principles, and if we had access to the ancestors, all 80 genera of traditional Flacourtiaceae would sink into one genus. The theory is all wrong. But when families are sunk on cladistic principles, the logical infrafamilial classification into monophyletic taxa is seldom considered. If you want a monophyletic system, you can have your wish, but only if you abolish ranks. It seems to me—and to many others—that cladistic classification into ranked taxa is both illogical in theory and disastrous in practice!

But there is still more bad news. Also in the cladogram we have the traditional **Salicaceae** (*Salix* L. and *Populus* L. with catkinate inflorescences, apetalous flowers, usually only two stamens in *Salix* and five in *Populus* against usually very many in traditional Flacourtiaceae, and distinctive fruits and seeds) nesting within the other major group of traditional Flacourts. So cladists again argue that it is essential to sink the family, and they call them tribe Saliceae. But the new tribe **Saliceae** nests within the tribe Flacourtieae, which is then just as paraphyletic as the family was. Again, sinking the family does not avoid paraphyly, and the traditional family Salicaceae must also sink to *below tribal level*. We have taxonomic free fall again. Characters are ignored. And again this is accompanied by a nomenclatural upheaval since in cladistic thinking the other half of the old Flacourtiaceae now has to be called Salicaceae, causing widespread confusion, and the name Flacourtiaceae falls into its synonymy. The name Salicaceae is now in use in two widely different senses. Many taxonomists would prefer to keep Flacourtiaceae in its traditional sense with three families apparently having evolved separately from within it, so we have a polyparaphyletic family. None of the three epiphyletic families had ever been sunk into Flacourtiaceae before on morphological grounds.

My next example is a group of families that used to constitute the order Primulales. Usually I don't query the mechanism for producing the cladogram, but when I find it is claimed that the arborescent tropical Myrsinaceae have evolved from the largely temperate herbaceous **Primulaceae** (Anderberg et al., 1998: 99), this seems to be the reverse of intuitive expectation, and I wonder if somebody should test the analysis again. Cladists, of course, recognized clades instead of taxa, and they at first combined one half of Primulaceae with Myrsinaceae, placing genera such as *Cyclamen* L. in Myrsinaceae (see Ståhl & Anderberg, 2004). Extraordinary indeed, but exactly the sort of thing that you might expect if only clades are recognized and characters are ignored. Later, the Angiosperm Phylogeny Group (2009) went a lot further and restored *Cyclamen* to its natural family by sinking the perfectly acceptable families **Myrsinaceae**, **Maesaceae**, **Theophrastaceae**, **Samolaceae**, and **Coridaceae** all into Primulaceae. This is typical of the excessive lumping that results when the holy grail of holophyly catches the imagination and characters are ignored. Again, no infrafamilial classification into only monophyletic taxa has been offered. And I must also observe that according to cladistic principles, 11 of the 23 genera of traditional Primulaceae should be sunk into other genera—six (including *Dodecatheon* L., *Soldanella* L., and the usually caespitose *Dionysia* Fenzl) into *Primula* L. (Mast et al., 2004), three into *Androsace* L., and two into *Lysimachia* L. I am getting that sinking feeling again. You can have a monophyletic system if you abandon ranks and ignore characters to produce a cladification, but in a taxonomic classification we need characters and ranks.

Another group that has suffered recently are Boraginales, now sunk by cladists into one family **Boraginaceae**. Within this is a very distinctive traditional family, **Lennoaceae**, with four parasitic species in two genera from California to Venezuela recognized in the revision by Yatskievych and Mason (1986). Parasitism alone does not necessarily make it a good family, but the 5- to 9-merous flowers, and the ovary of five to nine (to 16) carpels producing a fruit dehiscing by a circumscissile lid to reveal a pie chart of up to 28 wedge-shaped seeds cannot be accommodated in my concept of Boraginaceae. Scarcely less extraordinary is the sinking into Boraginaceae of **Hoplestigmataceae**, which has two western African tree species with a calyx of two to five irregular segments, nine to 14 corolla lobes, 20 to 25 stamens, and a drupe $\leq$ 3 cm long with a leathery exocarp and bony endocarp. Boraginaceae? No way! Also sunk are **Hydrophyllaceae**, with 15 genera and 300 species confined to the New World, which has virtually always been recognized as a separate family, and the African **Wellstediaceae**, with seven species in one

genus, which has also often been recognized. Both differ significantly from traditional Boraginaceae in having dehiscent capsules instead of four nutlets or fleshy pyrenes, and there is no need to sink these established families if you just accept the importance of characters and recognize paraphyletic taxa. Today I also recognize a family **Codonaceae** for one genus *Codon* L. (type) with two annual species from South Africa. It was recently rightly removed on morphological grounds from Hydrophyllaceae by Retief and van Wyk (2005), who made it a new subfamily Codonoideae in Boraginaceae (2005: 79), but it is very different from that family in its 10- to 12-merous (rather than 4- to 5-merous) flowers, many-seeded capsules (instead of four nutlets or pyrenes), both spinelike and glandular trichomes (unlike Boraginaceae), pollen with Ubisch bodies (as in Wellstediaceae), and other characters. Characters do matter in taxonomy.

If our taxonomy is too far removed from the intuitive appreciation of its users, they will just not accept it. An outstanding example is the sinking of **Valerianaceae**, **Dipsacaceae**, **Morinaceae**, and **Triplostegiaceae** into paraphyletic traditional **Caprifoliaceae**, but at least this is more inclined to provoke mere mirth rather than stringent criticism. It is sufficient to say that characters have again been ignored. The sinking into Malvaceae of nine families that have been recognized by Cheek (2007) in *Flowering Plant Families of the World*—**Sterculiaceae**, Pentapetaceae (now **Dombeyaceae** nom. conserv.), **Bombacaceae**, **Tiliaceae**, **Sparrmanniaceae**, **Brownlowiaceae**, **Byttneriaceae**, **Helicteraceae**, and **Durionaceae**—may not be an obvious case of paraphyly, but it is again the result of disregard of characters producing excessively broad taxa (Bayer et al., 1999). The lime tree, baobab, and durian do not sit comfortably in Malvaceae. If you want an Australian example, I could argue that it is not compulsory to sink herbaceous Tremandraceae into paraphyletic arborescent traditional **Elaeocarpaceae**, when the former has virtually none of the characters regularly quoted to characterize the latter.

The aquatic habitat is presumed to have provoked rapid evolution in many plants and so is likely to have produced good examples of paraphyletic taxa. The extraordinary aquatic family **Hydrostachyaceae**, one genus of 22 species widespread in fast-flowing water in the Old World tropics, is so weird that I cannot even work out how roots, stems, and leaves are to be distinguished. It is found in several different molecular analyses (see Albach et al., 2001) to nest with two New World genera of shrubs of **Hydrangeaceae** from the semidesert regions of the southwestern United States. But instead of sinking the family into Hydrangeaceae, and then logically into its tribe Philadelphieae (taxonomic free fall setting in again), those interested are now trying to find technical reasons to discount the several molecular analyses that put it there. It seems there are situations in which those adopting cladistic principles find the results too embarrassing to actually implement their conclusions.

A similar case concerns another family of fast-moving water, the **Podostemaceae**, where the habitat has again imposed a somewhat extreme morphological structure. It is agreed, perhaps surprisingly, that the family comes phylogenetically next to *Hypericum* L. (e.g., Davis & Chase, 2004), which most evolutionary taxonomists would place in **Clusiaceae**. But cladists involved decline to sink the nearly 50 genera of Podostemaceae into Clusiaceae, arguing instead that it is easier to recognize Hypericaceae (which few evolutionary taxonomists would agree with) and assume the Podostems will conveniently fall between that and Clusiaceae. This seems to me to be an unwarranted simplistic assumption relying excessively on cladogram topology and ignoring characters. Why can we not simply accept the family Podostemaceae (which has very many more distinctive characters than Hypericaceae would have) as evolutionary taxonomists have always done? The status of one taxon should not dictate the status of another. Podostemaceae did not arise from nothing by special creation; it evolved from within a different family, presumably Clusiaceae, which must be paraphyletic. No problem. Then *Hypericum* can stay in Clusiaceae.

Another case where it seems to be too much for cladists to actually accept their own principles is the potential sinking of **Cactaceae**—already made up of four subfamilies—into paraphyletic traditional **Portulacaceae**. Then logically, following taxonomic free fall again, it should sink to *below tribal level* in whichever tribe includes *Talinum* (classifications of the family vary; see Hershkovitz & Zimmer, 1997). Do we really need to sink four subfamilies together at a level lower than tribe? Again, the theory behind it is nonsensical. But Cactaceae is a high-profile family, and sinking it might make cladistic taxonomists look silly and cost them support among the general public. So they don't do it. Similarly a parallel succulent family in Madagascar and Africa, **Didiereaceae**, now divided into three subfamilies (Applequist & Wallace, 2003), also nests within the traditional Portulacaceae and on cladistic principles should also be sunk to *below tribal level* in that family. The alternative cladistic strategy, noted above, of splitting

the paraphyletic group rather than sinking another taxon into it, has resulted in the recent (Nyffeler & Eggli, 2010) dismemberment of the traditional Portulacaceae into several very narrowly defined families including **Montiaceae**, **Talinaceae**, and **Anacampserotaceae**, which does not seem helpful or desirable.

An extreme case of splitting concerns **Scrophulariaceae**. A first molecular analysis (based, it must be said, on the very limited sampling of 38 genera in a family of ca. 300) suggested that it should be split up into several clades that were to be treated as families (Olmstead et al., 2001), even though there were no characters quoted to justify this. More segregate families have been split off since, but I have not seen anybody try to key them out using *characters*. This seems to be a reversal of the principle behind the sinking of nine families into Malvaceae, referred to above. Why should we split in one case and sink in the other? Again, the importance of characters is ignored. And then other families where there do seem to be good characters, such as **Plantaginaceae**, **Hippuridaceae**, and **Callitrichaceae**, have had to be sunk on cladistic theory into Scroph segregates. And as in Flacourtiaceae, discussed above, awful nomenclatural upheavals follow. The name Plantaginaceae is still applied by many to a well-known family of three genera with very distinctive ovary structures, but it is now applied in cladistic literature to nearly 100 genera formerly referred to Scrophulariaceae. And at generic level, both *Bougueria* Decne. (producing a nut with a single peltate seed) and *Littorella* P. J. Bergius have been sunk into *Plantago* L. on cladistic principles (Schwarzbach, 2004). That might be good cladonomy if ranks were abandoned, but it is bad taxonomy. This sort of thing will always happen when completely different taxonomic principles are confused, and it is very disruptive.

Finally, perhaps we should raise our sights above the family level. For two centuries the flowering plants have been instinctively divided into dicots and monocots. Today it is not really doubted that the monocots are a monophyletic group, but it is established by molecular and other data that they have split off from dicot ancestors, leaving the **dicots** as a paraphyletic group. So our intuitive grouping of the flowering plants has been abandoned by the cladists, and the dicots are not recognized as a group distinct from the monocots. Are we not losing some useful taxonomy in all this? But if we have all the relevant information, we must realize that if the monocots are monophyletic, they must have arisen from within one *family* of dicots and so should be sunk completely into that. That is the logical conclusion of cladistic classification. We have taxonomic free fall waiting to happen again. And since the Rosids, Asterids, and Eudicots must have evolved from something, presumably at least the **Magnoliids** are also paraphyletic. We cannot escape paraphyly. See also Stuessy (2010).

## Conclusions

While the methodology of cladistic analysis has facilitated welcome new perspectives in taxonomy, and major advances in reconstructing phylogeny have been made recently by molecular methods, in our taxonomy we must resist the temptation to overemphasize these developments. There are many more examples I could give where cladistics has upset evolutionary family classification. Cases at generic rank are perhaps even more aggravating to the general public, and the controversial sinking of *Dryandra* R. Br. to a mere series of paraphyletic *Banksia* L. f. (taxonomic free fall again) is a current talking point here in Australia (see George, 2014, this issue). In my opinion cladistic classification into ranked taxa without any being paraphyletic has been the worst fad ever to hit taxonomy. The whole theory behind it is nonsensical, based on the logical impossibility of recognizing only complete clades as taxa and yet applying ranks to them. As a result, alas, characters are ignored, and much bad taxonomy is produced today. Whenever a modern revision claims that all taxa are now monophyletic (= holophyletic), suspicions are immediately aroused about the new taxonomy.

The impressive review of family classification by Cullen and Walters (2006) has raised the question of whether we can ever hope for a broadly agreed family list. They have emphasized that recent systems, though rightly taking account of new information from modern technologies, are not always the optimal result for users of taxonomy. They have tentatively suggested that a body could be set up, including both producers and users of taxonomy, to recommend an agreed list of families and to review this at alternate International Botanical Congresses (i.e., every 12 years). In principle this is an attractive idea, but at present it would be extremely difficult to achieve anything near general agreement. Nonetheless, it is worth thinking about. The question of monophyly versus characters should no doubt be high on the agenda. The taxonomic community has an obligation to respond to the needs of the users.

Cladistics disregards the importance of characters, fails to recognize newly evolved taxa, does not represent evolutionary reality, is increasingly disruptive of orthodox taxonomy, conflicts with natural

intuition, does not provide users with information they require, is ultimately a logical impossibility, and, above all, tends to produce bad taxonomy. But as this symposium on paraphyly shows, cladistic taxonomy with its illogical obsession with holophyly is now increasingly being challenged. Can we not ease cladistic taxonomy comfortably to a quiet resting place in biological history? Common sense and good taxonomy must inevitably return in due course.

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